Amendments to the Claims

This listing of claims will replace all prior versions and listings of all claims in the application.

Claims 1-27 (Cancelled)

28. (New) A method of screening for protozymes, said method comprising:

a) identifying a suitable protein scaffold lacking a desirable enzyme-like activity

b) inputting a protein backbone structure of said protein scaffold into a computer, wherein said backbone structure has variable residue positions;

c) inserting an active site domain into said scaffold comprising the use of one or more high energy state rotamers;

d) applying at least one protein design automation algorithm using high energy rotamers comprising:

i) establishing a group of variable position rotamers for each of said variable positions;

ii) analyzing the interaction of each said high energy rotamers with said variable position rotamers; and

iii) analyzing the interaction of each said high energy rotamers with the remainder of said protein backbone;

e) generating a set of candidate variant proteins with putative enzyme-like activity;

f) synthesizing a plurality of said candidate variant proteins with putative enzyme-like activity; and,

g) testing said candidate variant proteins with putative enzyme-like activity and selecting at least one of said candidate variant proteins with enzyme-like activity.

29. (New) A method according to claim 28 wherein said insertion step is done at the same time as applying said protein design automation algorithm.

30. (New) A method according to claim 28 further comprising applying a second protein design automation algorithm prior to said generating step.

31. (New) A method according to claim 28 wherein said active site domain catalyzes a known enzymatic reaction.

32. (New) A method according to claim 28 wherein said protein design automation algorithm comprises a DEE computation

33. (New) A method according to claim 28 wherein said protein design cycle includes the use of at least one scoring function.

34. (New) A method according to claim 33 wherein said scoring function is selected from the group consisting of a van der Waals potential scoring function, a hydrogen bond potential scoring function, an atomic solvation scoring function, an electrostatic scoring function and a secondary structure propensity scoring function.

35. (New) A method according to claim 28 wherein said synthesizing includes a shuffling step.

36. (New) A method according to claim 28 wherein said protein design algorithm comprises a force field calculation.